

GGGCCTAGGG CGCCGGGTCA GGGGCTCGA GATCGGGCTT GGGCCAGAG C ATG TTC	57
Met Phe	
1	
CAG ATC CCA GAG TTT GAG CCG AGT GAG CAG GAA GAC TCC AGC TCT GCA	105
Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser Ser Ala	
5 10 15	
GAG AGG GGC CTG GGC CCC AGC CCC GCA GGG GAC GGG CCC TCA GGC TCC	153
Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser Gly Ser	
20 25 30	
GGC AAG CAT CAT CGC CAG GCC CCA GGC CTC CTG TGG GAC GCC AGT CAC	201
Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala Ser His	
35 40 45 50	
CAG CAG GAG CAG CCA ACC AGC AGC AGC CAT CAT GGA GGC GCT GGG GCT	249
Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala Gly Ala	
55 60 65	
GTG GAG ATC CGG AGT CGC CAC AGC TCC TAC CCC GCG GGG ACG GAG GAC	297
Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr Glu Asp	
70 75 80	
GAC GAA GGG ATG GGG GAG GAG CCC AGC CCC TTT CGG GGC CGC TCG CGC	345
Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg Ser Arg	
85 90 95	
TCG GCG CCC CCC AAC CTC TGG GCA GCA CAG CGC TAT GGC CGC GAG CTC	393
Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu	
100 105 110	
CGG AGG ATG AGT GAC GAG TTT GTG GAC TCC TTT AAG AAG GGA CTT CCT	441
Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly Leu Pro	
115 120 125 130	
CGC CCG AAG AGC GCG GGC ACA GCA ACG CAG ATG CGG CAA AGC TCC AGC	489
Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser Ser Ser	
135 140 145	
TGG ACG CGA GTC TTC CAG TCC TGG TGG GAT CGG AAC TTG GGC AGG GGA	537
Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly Arg Gly	
150 155 160	

Fig. 1A

AGC TCC GCC CCC TCC CAG TGACCTTCGG TCCACATCCC GAAATCCACC	585
Ser Ser Ala Pro Ser Gln	
165	
CGTTCCCATTT GCCCTGGGCA GCCATTTTGA ATATGGGAGG AAGTAAGTTC CCTCAGGCCT	645
ATGCAAAAAG AGGATCCGTG CTGTATCCTT TGGAGGGAGG GTTGACCCAG ATTCCCTTCC	705
GGTGTGTGTG AAGCCACGGA AGGTTGGTCC CATCGGAAGT TTTGGGTTTT CCGCCCACAG	765
CCGCCGGAAG TGGCTCCGTG GCCCCGCCCT CAGGTTCCGG GGTTCCTCCC AGGCGCCTGC	825
GCTAAGTAGC GAGCCAGGTT TAACCGTTGT GTCACCGGGA CCCGAGCCCC CGCGATGCCC	885
TGGGGGCCGT GATCAGTACC AAATGTTAAT AAAGCCCGCG TGTGTGCCAA AAAAAAAAAA	945
A	946

Fig. 1B

10 20 30 40
1 MGTPKQPS LAPAHALGLRKSDPGIRSLGSDAGGRWRPAA PmBad
1 - - - - - PBM1

50 60 70 80
41 QSMFQIPEFEPSEQEDASATDRGLGPSLTEDQPGPY - - - PmBad
1 - - MFQIPEFEPSEQEDSSSAERGLGPS PAGDGPS GSGKHH PBM1

90 100 110 120
77 - LAPGLLGSNIHQQGRAAATNSHHGGAGAMETRSRHSSYPAPmBad
39 RQAPGLLWDASHQQEQPTSSSHHHGGAGAVEIRSRHSSYPAPBM1

130 140 150 160
116 GTEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMT PmBad
79 GTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMS PBM1

170 180 190 200
156 DEFEGSFK-GLPRPKSAGTATQMRQSAGWTRI IQSWWDRN PmBad
119 DEFVD SFFKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRN PBM1

210
195 LGKGGSTPSQ PmBad
159 LGRGSSAPSQ PBM1

Fig. 2

Bad 2-Hybrid Interactions

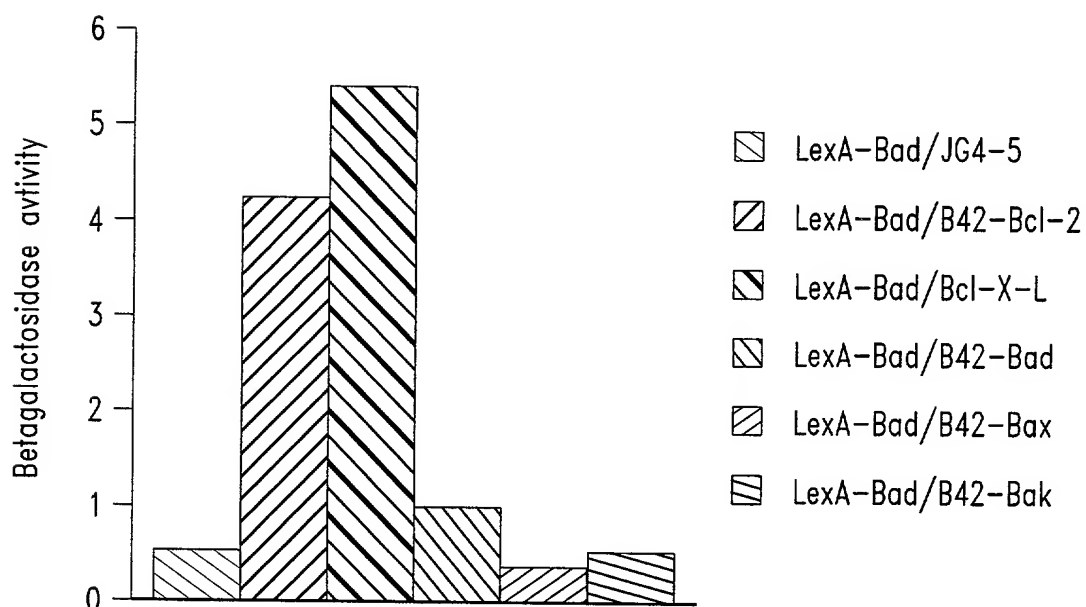


Fig. 3

Binding of Bcl-2 Family Proteins to Bad

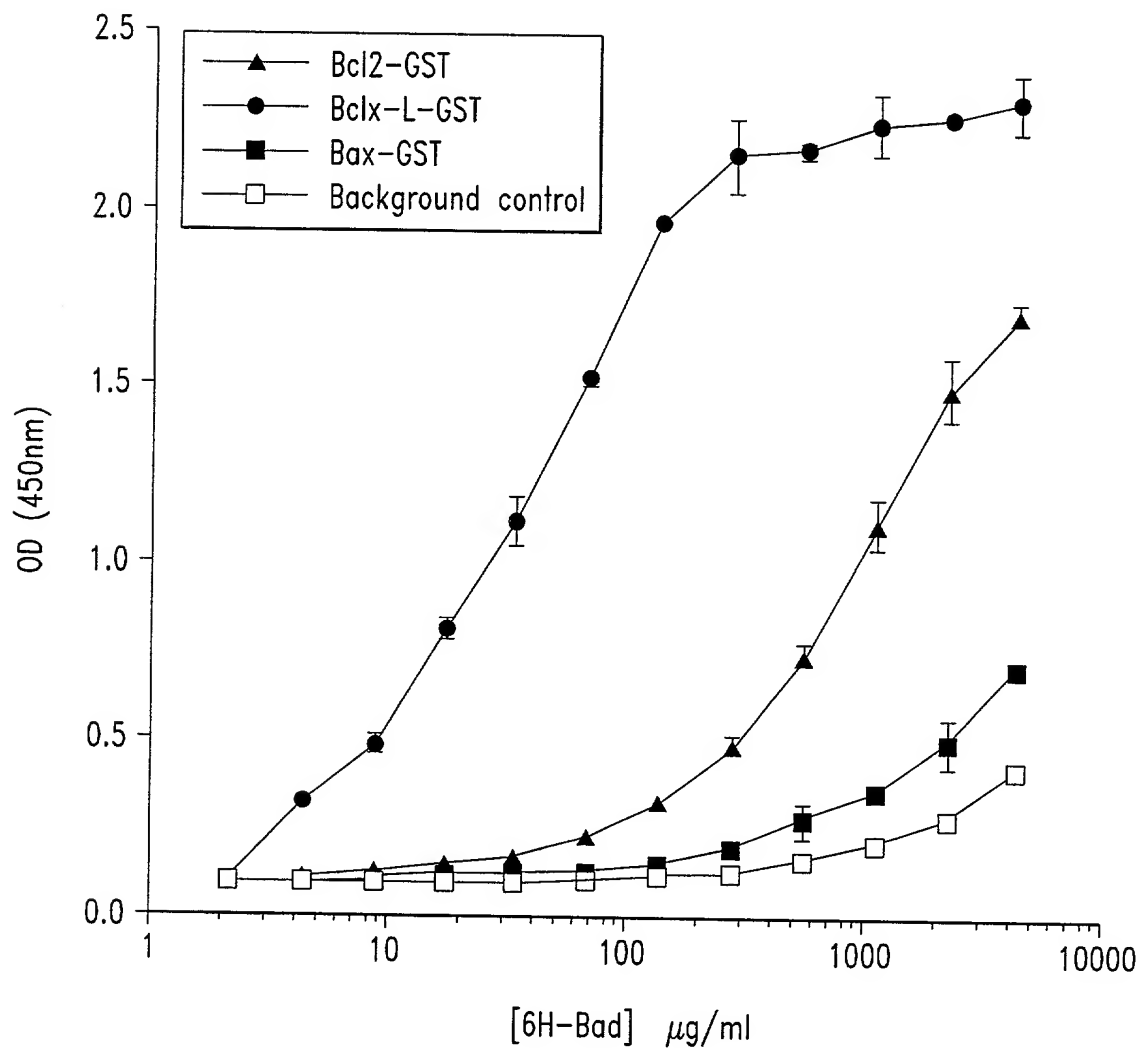


Fig. 4